=> d

L1 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2003 ACS on STN
RN **37318-43-7** REGISTRY
CN Isomerase, phosphoribosylformiminoaminophosphoribosylimidazolecarboxamide (9CI) (CA INDEX NAME)
OTHER NAMES:
CN E.C. 5.3.1.16
CN N'-(5'-Phosphoribosylformimino)-5-aminoimidazole-4-carboxamide ribonucleotide isomerase
CN N-(5'-Phospho-D-ribosylformimino)-5-amino-1-(5''-phosphoribosyl)-4-imidazolecarboxamide isomerase
CN Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase
CN Phosphoribosylformiminoaminophosphoribosylimidazolecarboxamide isomerase
CN ProFAR isomerase
DR 9075-36-9
MF Unspecified
CI MAN
LC STN Files: BIOSIS, CA, CAPLUS, TOXCENTER, USPATFULL

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
32 REFERENCES IN FILE CA (1907 TO DATE)
32 REFERENCES IN FILE CAPLUS (1907 TO DATE)

=> d ibib ab 1-17

L5 ANSWER 1 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1998:791955 HCAPLUS
DOCUMENT NUMBER: 130:205720
TITLE: A histidine gene cluster of the hyperthermophile Thermotoga maritima: sequence analysis and evolutionary significance
AUTHOR(S): Thoma, Ralf; Schwander, Martin; Liebl, Wolfgang; Kirschner, Kasper; Sterner, Reinhard
CORPORATE SOURCE: Abteilung fur Biophys. Chem., Biozentrum der Univ. Basel, Basel, CH-4056, Switz.
SOURCE: Extremophiles (**1998**), 2(4), 379-389
CODEN: EXTRFI; ISSN: 1431-0651
PUBLISHER: Springer-Verlag Tokyo
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The sequences of histidine operon genes in hyperthermophiles are informative for understanding high protein thermostability and the evolution of metabolic pathways. Therefore, a cluster of eight his genes from the hyperthermophilic and phylogenetically early bacterium Thermotoga maritima was cloned and sequenced. The cluster has the gene order hisDCBdHAFI-E, lacking only hisG and hisBp, and does not contain intercistronic regions. This compact organization of his genes resembles the his operon of enterobacteria. Sequence anal. downstream of the stop codon of hisI-E identifies a region with a significantly higher cytosine over guanosine content, which is indicative of a rho-dependent termination of transcription of the his operon. Multiple sequence alignments of N1-((5'-phosphoribosyl)-formimino)-5-aminoimidazole-4-carboxyamide ribonucleotide isomerase (HisA) and of the cycloligase moiety of imidazoleglycerol phosphate synthase (HisF) support the previous assignment of (.beta..alpha.)5-barrel fold to these proteins. The alignments also reveal a second phosphate-binding motif located in the first halves of both enzymes and thereby support the hypothesis that HisA and HisF have evolved by a sequence of two gene duplication events. Comparison of the amino acid compns. of HisA and HisF from mesophiles and thermophiles shows that the thermostable variants of both enzymes contain a significantly increased no. of charged amino acid residues and may therefore be stabilized by addnl. salt bridges.
REFERENCE COUNT: 54 THERE ARE 54 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 2 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1998:765429 HCAPLUS
DOCUMENT NUMBER: 130:120318
TITLE: Molecular cloning and characterization of the gene encoding N'-[(5'-phosphoribosyl)-formimino]-5-aminoimidazole-4-carboxamide ribonucleotide (BBM II) isomerase from Arabidopsis thaliana
AUTHOR(S): Fujimori, K.; Tada, S.; Kanai, S.; Ohta, D.
CORPORATE SOURCE: Takarazuka Research Institute, Novartis Pharma K.K, Takarazuka, 665, Japan
SOURCE: Molecular & General Genetics (**1998**), 259(2), 216-223
CODEN: MGGEAE; ISSN: 0026-8925
PUBLISHER: Springer-Verlag
DOCUMENT TYPE: Journal
LANGUAGE: English
AB An Arabidopsis BBM II isomerase cDNA was isolated from an Arabidopsis cDNA library by functional complementation of the Escherichia coli hisA mutant strain HfrG6. The isolated cDNA encodes a polypeptide of 304 amino acids with a calcd. mol. wt. of 33,363. Sequence comparison with the HIS6 proteins of yeasts revealed that Arabidopsis BBM II isomerase contains an N-terminal extension of .apprx.40 amino acids that shows the general properties of chloroplast transit peptides. This finding is consistent with the localization of other histidine biosynthetic enzymes, such as imidazoleglycerolphosphate dehydratase and histidinol dehydrogenase, in the chloroplasts in higher plants. The primary structure of the mature protein was 50 and 42% identical, resp., to the HIS6 proteins of

Schizosaccharomyces pombe and Saccharomyces cerevisiae, resp., while no prominent sequence similarity to the bacterial BBM II isomerase was found. That the isolated Arabidopsis cDNA actually encodes a functionally active BBM II isomerase activity was confirmed in an in vitro enzyme assay using a crude ext. prepd. from strain HfrG6 transformed with the Arabidopsis BBM II isomerase cDNA.

REFERENCE COUNT: 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 3 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1998:694554 HCAPLUS
DOCUMENT NUMBER: 130:61862
TITLE: Buchnera aphidicola (aphid endosymbiont) contains genes encoding enzymes of histidine biosynthesis
AUTHOR(S): Clark, Marta A.; Baumann, Linda; Baumann, Paul
CORPORATE SOURCE: Microbiology Section, University of California, Davis, CA, 95616-8665, USA
SOURCE: Current Microbiology (**1998**), 37(5), 356-358
CODEN: CUMIDD; ISSN: 0343-8651
PUBLISHER: Springer-Verlag New York Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Buchnera aphidicola is an endosymbiont of aphids. One of its functions appears to be the synthesis of essential amino acids for the aphid host. A 12.8-kilobase B. aphidicola DNA fragment has been cloned and sequenced. It contains genes encoding all of the enzymes required for the biosynthesis of the essential amino acid histidine. The order of the genes, hisGDCBHAFI, is the same as that found in Escherichia coli and is consistent with their constituting a single transcription unit. The DNA fragment also contained genes involved in arom. amino acid biosynthesis (aroC), the oxidative pentose pathway (gnd), and 2'-deoxyribonucleotide metab. (dcd), as well as a tRNA synthase (metG).

REFERENCE COUNT: 16 THERE ARE 16 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 4 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1998:429128 HCAPLUS
DOCUMENT NUMBER: 129:171257
TITLE: Cloning of the histidine biosynthetic genes of Corynebacterium glutamicum: organization and sequencing analysis of the hisA, impA, and hisF gene cluster
AUTHOR(S): Jung, Sam-Il; Han, Myeong-Sin; Kwon, Joon-hye; Cheon, Choong-Ill; Min, Kyung-Hee; Lee, Myeong-Sok
CORPORATE SOURCE: Department of Biological Science, Sookmyung Women's Univ., Seoul, 140-742, S. Korea
SOURCE: Biochemical and Biophysical Research Communications (**1998**), 247(3), 741-745
CODEN: BBRCA9; ISSN: 0006-291X
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The hisA and hisF genes of Corynebacterium glutamicum were cloned by transforming histidine auxotrophic Escherichia coli with the genomic DNA library. They are two of the eight genes that participate in the histidine biosynthetic pathway. Cloned DNA fragments contg. the genes can also complement hisH and hisI auxotrophs of Escherichia coli, suggesting that the four genes are clustered in the genome. The authors detd. the nucleotide sequences of the minimal fragment contg. the hisA and hisF genes, which are sepd. by the impA gene. The coding regions of the hisA and hisF genes are 245 and 257 amino acids in length with a predicted size of about 26 and 27 kDa, resp. These are in good agreements with the sizes of proteins expressed in E. coli. A high similarity was obsd. in comparison of nucleotide sequences of each protein between C. glutamicum and other species, as well as those between hisA and hisF genes of fC. glutamicum. (c) 1998 Academic Press.

REFERENCE COUNT: 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 5 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1998:105638 HCAPLUS
DOCUMENT NUMBER: 128:240142
TITLE: Isolation and characterization of Rhodobacter capsulatus mutants affected in cytochrome cbb3 oxidase activity
AUTHOR(S): Koch, Hans-Georg; Hwang, Olivia; Daldal, Fevzi
CORPORATE SOURCE: Department of Biology, Plant Science Institute, University of Pennsylvania, Philadelphia, PA, 19104-6018, USA
SOURCE: Journal of Bacteriology (**1998**), 180(4), 969-978
CODEN: JOBAAY; ISSN: 0021-9193
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The facultative phototrophic bacterium Rhodobacter capsulatus contains only one form of cytochrome (cyt) c oxidase, which has recently been identified as a cbb3-type cyt c oxidase. This is unlike other related species, such as Rhodobacter sphaeroides and Paracoccus denitrificans, which contain an addnl. mitochondrial-like aa3-type cyt c oxidase. An extensive search for mutants affected in cyt c oxidase activity in R. capsulatus led to the isolation of at least five classes of mutants. Plasmids complementing them to a wild-type phenotype were obtained for all but one of these classes from a chromosomal DNA library. The first class of mutants contained mutations within the structural genes (ccoNOQP) of the cyt cbb3 oxidase. Sequence anal. of these mutants and of the plasmids complementing them revealed that ccoNOQP in R. capsulatus is not flanked by the oxygen response regulator fnr, which is located upstream of these genes in other species. Genetic and biochem. characterizations of mutants belonging to this group indicated that the subunits CcoN, CcoO, and CcoP are required for the presence of an active cyt cbb3 oxidase, and unlike in Bradyrhizobium japonicum, no active CcoN-CcoO subcomplex was found in R. capsulatus. In addn., mutagenesis expts. indicated that the highly conserved open reading frame 277 located adjacent to ccoNOQP is required neither for cyt cbb3 oxidase activity or assembly nor for respiratory or photosynthetic energy transduction in R. capsulatus. The remaining cyt c oxidase-minus mutants mapped outside of ccoNOQP and formed four addnl. groups. In one of these groups, a fully assembled but inactive cyt cbb3 oxidase was found, while another group had only extremely small amts. of it. The next group was characterized by a pleiotropic effect on all membrane-bound c-type cytochromes, and the remaining mutants not complemented by the plasmids complementing the first four groups formed at least one addnl. group affecting the biogenesis of the cyt cbb3 oxidase of R. capsulatus.
REFERENCE COUNT: 59 THERE ARE 59 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 6 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1997:555491 HCAPLUS
DOCUMENT NUMBER: 127:288789
TITLE: Paralogous histidine biosynthetic genes: evolutionary analysis of the Saccharomyces cerevisiae HIS6 and HIS7 genes
AUTHOR(S): Fani, Renato; Tamburini, Elena; Mori, Elena; Lazcano, Antonio; Lio, Pietro; Barberio, Claudia; Casalone, Enrico; Cavalieri, Duccio; Perito, Brunella; Polsinelli, Mario
CORPORATE SOURCE: Dipartimento di Biologia Animale e Genetica, Universita degli Studi di Firenze, Via Romana 17, I-50125, Florence, Italy
SOURCE: Gene (**1997**), 197(1/2), 9-17
CODEN: GENED6; ISSN: 0378-1119
PUBLISHER: Elsevier
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The HIS6 gene from Saccharomyces cerevisiae strain YNN282 is able to complement both the S. cerevisiae his6 and the Escherichia coli hisA mutations. The cloning and the nucleotide sequence indicated that this

gene encodes a putative phosphoribosyl-5-amino-1-phosphoribosyl-4-imidazolecarboxiamide isomerase (5' Pro-FAR isomerase, EC 5.3.1.16) of 261 amino acids, with a mol. wt. of 29554. The HIS6 gene product shares a significant degree of sequence similarity with the prokaryotic HisA proteins and HisF proteins, and with the C-terminal domain of the S. cerevisiae HIS7 protein (homologous to HisF), indicating that the yeast HIS6 and HIS7 genes are paralogous. Moreover, the HIS6 gene is organized into two homologous modules half the size of the entire gene, typical of all the known prokaryotic hisA and hisF genes. The structure of the yeast HIS6 gene supports the two-step evolutionary model suggested by Fani et al. (J. Mol. Evol. 1994; 38: 489-495) to explain the present-day hisA and hisF genes. According to this idea, the hisF gene originated from the duplication of an ancestral hisA gene which, in turn, was the result of an earlier gene elongation event involving an ancestral module half the size of the extant gene. Results reported in this paper also suggest that these two successive paralogous gene duplications took probably place in the early steps of mol. evolution of the histidine pathway, well before the diversification of the three domains, and that this pathway was one of the metabolic activities of the last common ancestor. The mol. evolution of the yeast HIS6 and HIS7 genes is also discussed.

REFERENCE COUNT: 52 THERE ARE 52 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 7 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1997:283820 HCAPLUS
DOCUMENT NUMBER: 126:260140
TITLE: Metal contaminants removal from soil or other substrates using transgenic plants engineered to contain increased histidine levels for metal uptake and tolerance
INVENTOR(S): Smith, James Andrew Charles; Kramer, Ute; Baker, Alan John Martin
PATENT ASSIGNEE(S): Isis Innovation Limited, UK; Smith, James Andrew Charles; Kramer, Ute; Baker, Alan John Martin
SOURCE: PCT Int. Appl., 37 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9710346	A2	19970320	WO 1996-GB2264	19960912 <--
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG				
AU 9669385	A1	19970401	AU 1996-69385	19960912 <--
EP 871750	A2	19981021	EP 1996-930273	19960912 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
US 2002157128	A1	20021024	US 1998-29941	19980416

PRIORITY APPLN. INFO.: GB 1995-18599 A 19950912
WO 1996-GB2264 W 19960912

AB This invention comprises materials and methods for removing metal pollutants from metal-contg. substrates, particularly soil environments using plants modified so as to contain an increased concn. of the amino acid histidine responsible for metal uptake and tolerance. Plants were engineered to contain increased levels of histidine by transformation with Escherichia coli gene hisB, hisD, or hisG, for example. These genes encode imidazole glycerol phosphate dehydratase, histidinol dehydrogenase, and ATP phosphoribosyltransferase phosphoribosyl-ATP phosphohydrolase, resp. Brassica oleracea was the plant transformed with E. coli genes.

L5 ANSWER 8 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1996:505343 HCAPLUS
DOCUMENT NUMBER: 125:163482
TITLE: A spatial analysis of physiological changes associated with infection of cotyledons of marrow plants with cucumber mosaic virus
AUTHOR(S): Tecsi, Laszlo I.; Smith, Alison M.; Maule, Andrew J.; Leegood, Richard C.
CORPORATE SOURCE: Robert Hill Inst., Dep. Animal Plant Sciences, Univ. Sheffield, Sheffield, S10 2TN, UK
SOURCE: Plant Physiology (**1996**), 111(4), 975-985
CODEN: PLPHAY; ISSN: 0032-0889
PUBLISHER: American Society of Plant Physiologists
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Changes in host primary metab. assocd. with the compatible interaction between cucumber mosaic virus and cotyledons of the marrow plant (Cucurbita pepo L.) have been localized, first by measuring activities of key enzymes in infected and uninfected regions of the cotyledon, and second by histochem. techniques applied to tissue prints of the infected region. A series of progressive metabolic changes occurs within the expanding infected lesion. Virus replication and the synthesis of viral protein at the periphery creates a strong sink demand assocd. with increased activities of anaplerotic enzymes, increased photosynthesis, and starch accumulation. Inside the lesion, when the synthesis of virus has declined, photosynthesis is reduced, starch is mobilized, and the emphasis of metab. is shifted toward glycolysis and mitochondrial respiration. These changes are assocd. spatially with the onset of chlorosis. A decrease in total protein synthesis in this inner zone could be instrumental in some or all of these changes, leading to symptoms of viral infection.

L5 ANSWER 9 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1995:937211 HCAPLUS
DOCUMENT NUMBER: 124:48625
TITLE: Inverse protein folding by the residue pair preference profile method: estimating the correctness of alignments of structurally compatible sequences
AUTHOR(S): Wilmanns, Matthias; Eisenberg, David
CORPORATE SOURCE: UCLA-DOE Laboratory of Structural Biology, University of California at Los Angeles, Los Angeles, CA, 90024-1570, USA
SOURCE: Protein Engineering (**1995**), 8(7), 627-39
CODEN: PRENE9; ISSN: 0269-2139
PUBLISHER: Oxford University Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The residue pair preference profile (R3P) method is an inverse folding method that combines environmental profiles and pair preference profiles. The method uses statistical preferences for residue pairs which score the likelihood of finding a profiled residue to be paired with a residue within its local environment. All pairs are characterized by their dihedral angles, secondary structure, and no. of neighboring residues as a function of residue type. Each residue pair preference is expressed for all 20 amino acids of the profiled residue and is weighted by the compatibility of the environment residue with its own local environment. The R3P method produces an initial profile-sequence alignment which is then refined by converting the initial profile into a profile of a target sequence threaded into the structure of the initial profile. This method was tested by evaluating alignments of sequences with known 3-dimensional structures using structural superposition alignments as ref. R3P-sequence alignments are .gtoreq.50% correct on av. for sequences whose 3-dimensional structure pairs superimpose with an r.m.s. deviation of .ltoreq.1.97 .ANG.. The av. improvement in correctness during this iterative refinement is 14%. The R3P-sequence alignments are compared with sequence-sequence and 3-D profile-sequence alignments. When all 3 methods are combined, on av. .gtoreq.50% of the alignments are correct for pairs of 3-dimensional structures that superimpose within 2.12 .ANG.. A 3-dimensional model of HisA is predicted with the combined method.

L5 ANSWER 10 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1994:451270 HCAPLUS
DOCUMENT NUMBER: 121:51270
TITLE: The evolution of the histidine biosynthetic genes in prokaryotes: a common ancestor for the hisA and hisF genes
AUTHOR(S): Fani, Renato; Lio, Pietro; Chiarelli, Ilaria; Bazzicalupo, Marco
CORPORATE SOURCE: Dip. Biol. Anim. Genet., Univ. Studi, Firenze, 50125, Italy
SOURCE: Journal of Molecular Evolution (**1994**), 38(5), 489-95
CODEN: JMEVAU; ISSN: 0022-2844
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The hisA and hisF genes belong to the histidine operon that has been extensively studied in the enterobacteria Escherichia coli and Salmonella typhimurium where the hisA gene codes for the phosphoribosyl-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase (EC 5.3.1.16) catalyzing the 4th step of the histidine biosynthetic pathway, and the hisF gene codes for a cyclase catalyzing the 6th reaction. Comparative anal. of nucleotide and predicted amino acid sequences of hisA and hisF genes in different microorganisms showed extensive sequence homol. (43% considering similar amino acids), suggesting that the 2 genes arose from an ancestral gene by duplication and subsequent evolutionary divergence. A more detailed anal., including mutual information, revealed an internal duplication both in hisA and hisF genes in each of the considered microorganisms. The authors propose that the hisA and hisF have originated from the duplication of a smaller ancestral gene corresponding to half the size of the actual genes followed by rapid evolutionary divergence. The involvement of gene elongation, gene duplication, and gene fusion in the evolution of the histidine biosynthetic genes is also discussed.

L5 ANSWER 11 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1993:164696 HCAPLUS
DOCUMENT NUMBER: 118:164696
TITLE: Three-dimensional profiles from residue-pair preferences: Identification of sequences with .beta./.alpha.-barrel fold
AUTHOR(S): Wilmanns, Matthias; Eisenberg, David
CORPORATE SOURCE: Mol. Biol. Inst., Univ. California, Los Angeles, CA, 90024-1570, USA
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (**1993**), 90(4), 1379-83
CODEN: PNASA6; ISSN: 0027-8424
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The 3-dimensional (3D) profile method expresses the 3D structure of a protein as a table, the profile, which represents the local environment of each residue. The score of an amino acid sequence, aligned with the 3D profile, reflects its compatibility with the profiled structure. In the original implementation, each local environment was characterized by its polarity, the area buried of its side chain, and its secondary structure. Here is described a modified 3D profile algorithm that characterizes the local environment in terms of the statistical preferences of the profiled residue for neighbors of specific residue types, main-chain conformations, or secondary structure. Combined profiles of the original and the 3 new types were tested on .beta./.alpha.-barrel protein structures. The method identified the following enzymes of unknown 3D structure as probable .beta./.alpha.-barrels, all of which catalyze reactions in the biosynthesis of arom. amino acids: anthranilate phosphoribosyltransferase (trpD), glutamine amidotransferase (trpG), and **phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase** (hisA).

L5 ANSWER 12 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1991:599836 HCAPLUS

DOCUMENT NUMBER: 115:199836
TITLE: Cloning and characterization of the histidine biosynthetic gene cluster of Streptomyces coelicolor A3(2) [Erratum to document cited in CA114(3):18171p]
AUTHOR(S): Limauro, Danila; Avitabile, Alessandra; Cappellano, Carmela; Puglia, Anna Maria; Bruni, Carmelo B.
CORPORATE SOURCE: Cent. Endocrinol. Oncol. Sper., CNR, Naples, 80131, Italy
SOURCE: Gene (**1991**), 101(1), 161-2
CODEN: GENED6; ISSN: 0378-1119
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A portion of Figure 4, omitted from the original article, has been provided. The error was not reflected in the abstr. or the index entries.

L5 ANSWER 13 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1991:222340 HCAPLUS
DOCUMENT NUMBER: 114:222340
TITLE: Physical and genetic map of the Methanococcus voltae chromosome
AUTHOR(S): Sitzmann, J.; Klein, A.
CORPORATE SOURCE: Fachbereich Biol., Philipps-Univ., Marburg, D-3550, Germany
SOURCE: Molecular Microbiology (**1991**), 5(2), 505-13
CODEN: MOMIEE; ISSN: 0950-382X
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A phys. map of the M. voltae chromosome was constructed on the basis of restriction mapping and cross-hybridization expts., employing total and partial digests obtained with rarely cutting restriction enzymes. On the basis of the sum of the fragment sizes of digests with 7 enzymes the chromosome length was calcd. to be .apprx.1900 kb. The derived map is circular. Hybridization of gene probes to mapped restriction fragments has led to a genetic map of genes for structural RNAs as well as proteins, including enzymes involved in the methanogenic pathway.

L5 ANSWER 14 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1991:18171 HCAPLUS
DOCUMENT NUMBER: 114:18171
TITLE: Cloning and characterization of the histidine biosynthetic gene cluster of Streptomyces coelicolor A3(2)
AUTHOR(S): Limauro, Danila; Avitabile, Alessandra; Cappellano, Carmela; Puglia, Anna Maria; Bruni, Carmelo B.
CORPORATE SOURCE: Cent. Endocrinol. Oncol. Sper., CNR, Naples, 80131, Italy
SOURCE: Gene (**1990**), 90(1), 31-41
CODEN: GENED6; ISSN: 0378-1119
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Biochem. and genetic data indicate that in S. coelicolor A3(2) the majority of the genes involved in the biosynthesis of histidine are clustered in a small region of the chromosome. To investigate the structural organization and the regulation of these genes, genomic libraries from S. coelicolor A3(2) were constructed in pUC vectors. Recombinant clones were isolated by complementation of an Escherichia coli hisBd auxotroph. A recombinant plasmid contg. a 3.4-kb fragment of genomic DNA was further characterized. When cloned in the plasmid vector, pIJ699, this fragment was able to complement S. coelicolor A3(2) hisB mutants. Overlapping clones spanning a 15-kb genomic region were isolated by screening other libraries with labeled DNA fragments obtained from the first clone. Deriv. clones were able to complement mutations in 4 different cistrons of the his cluster of S. coelicolor A3(2). Nucleotide sequence anal. of a 4-kb region allowed the identification of 5 ORFs which showed significant homol. with the his gene products of E. coli. The order of the genes in S. coelicolor A3(2) (5'-hisD-hisC-hisBd-hisH-hisA-3') is the same as in the -is operon of E. coli.

L5 ANSWER 15 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1990:112949 HCAPLUS
DOCUMENT NUMBER: 112:112949
TITLE: Structure and function of the Salmonella typhimurium and Escherichia coli K-12 histidine operons
AUTHOR(S): Carlomagno, Maria Stella; Chiariotti, Lorenzo; Alifano, Pietro; Nappo, Anna Giulia; Bruni, Carmelo B.
CORPORATE SOURCE: Dip. Biol. Patol. Cell. Mol., Univ. Naples, Naples, 80131, Italy
SOURCE: Journal of Molecular Biology (**1988**), 203(3), 585-606
CODEN: JMOBAK; ISSN: 0022-2836
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The complete nucleotide sequence of the histidine operons of E. coli and S. typhimurium were detd. This structural information enabled investigation of the expression and organization of the histidine operon. The proteins coded by each of the putative histidine cistrons were identified by subcloning appropriate DNA fragments and by analyzing the polypeptides synthesized in minicells. A structural comparison of the gene products was performed. The histidine mRNA mols. produced in vivo and the internal transcription initiation sites were identified by Northern blot anal. and S1 nuclease mapping. A comparative anal. of the different transcriptional and translational control elements within the 2 operons reveals a remarkable preservation for most of them except for the intercistronic region between the first (hisG) and second (hisD) structural genes and for the rho-independent terminator of transcription at the end of the operon. Overall, the operon structure if very compact and its expression appears to be regulated at several levels.

L5 ANSWER 16 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1985:482550 HCAPLUS
DOCUMENT NUMBER: 103:82550
TITLE: Structure and sequence divergence of two archaebacterial genes
AUTHOR(S): Cue, David; Beckler, Gregory S.; Reeve, John N.; Konisky, Jordan
CORPORATE SOURCE: Dep. Microbiol., Univ. Illinois, Urbana, IL, 61801, USA
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (**1985**), 82(12), 4207-11
CODEN: PNASA6; ISSN: 0027-8424
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The DNA sequences of a region that includes the hisA gene of 2 related methanogenic archaebacteria, Methanococcus voltae and M. vannielii, have been compared. Both organisms show a similar genome organization in this region, displaying 2 open reading frames (ORFs) sepd. by regions of very high A+T content. Two of the ORFs, including ORFHisA, show significant DNA sequence homol. As might be expected for organisms having a genome that is A+T-rich, there is a high preference for A and U as the 3rd base in codons. Although the regions upstream of the structural genes contain prokaryotic-like promoter sequences, it is not known whether they are recognized as promoters in these archaebacterial cells. A ribosome binding site, G-G-T-G, is located 6 base pairs preceding the ATG translation initiation sequence of both hisA genes. The sequences upstream of the 2 hisA genes show only limited sequence homol. The M. voltae intergenic region contains four tandemly arranged repetitions of an 11-base-pair sequence, whereas the M. vannielii sequence contains both direct and inverted repetitive sequences. Based on the degree of hisA sequence homol., it is concluded that M. voltae and M. vannielii are less closely related taxonomically than are members of the enteric group of eubacteria.

L5 ANSWER 17 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1972:55706 HCAPLUS
DOCUMENT NUMBER: 76:55706
TITLE: Enzymes and intermediates of histidine biosynthesis in Salmonella typhimurium

AUTHOR(S): Martin, Robert G.; Berberich, Mary A.; Ames, Bruce N.; Davis, Warren W.; Goldberger, Robert F.; Yourno, Joseph D.
CORPORATE SOURCE: Natl. Inst. Health, Bethesda, MD, USA
SOURCE: Methods Enzymol. (**1971**), Volume 17, Issue Pt. B, 3-44. Editor(s): Colowick, S. P. Academic: New York, N. Y.
CODEN: 18HWA8
DOCUMENT TYPE: Conference
LANGUAGE: English
AB Chem. and phys. characteristics of the 10 enzymes involved in histidine biosynthesis in S. typhimurium are given with methods and precautions for their assay.